

BLAST Basic Local Alignment Search ToolSEQ 2

Job Title: BD205212:Nucleotide sequence for detecting...

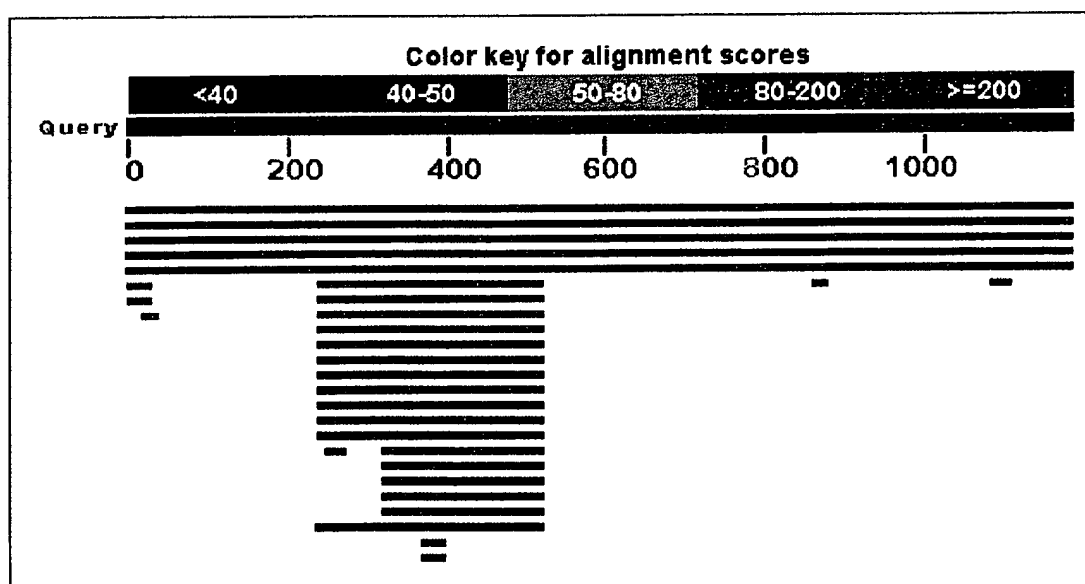
Document 2

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BLASTN 2.2.18+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402. RID: 88NSGD54014 Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences) 7,064,549 sequences; 24,305,219,031 total letters

Query= gi|33014982|dbj|BD205212.1| Nucleotide sequence for detecting enterohemorrhagic Escherichia coli (EHEC) Length=1181

Distribution of 30 Blast Hits on the Query Sequence

Distance tree of results **NEW**Legend for links to other resources: **U** UniGene **E** GEO **G** Gene **S** Structure**Sequences producing significant alignments:**

(Click headers to sort columns)

AF401292.1	Escherichia coli O157:H- plasmid pSF0157, complete sequence	2111	2111	100%	0.0	99%	
AF074613.1	Escherichia coli O157:H7 plasmid p0157, complete sequence	2111	2111	100%	0.0	99%	
Y11275.1	E.coli 7.4 kb DNA from plasmid p0157	2111	2111	100%	0.0	99%	G
AB011549.2	Escherichia coli O157:H7 str. Sakai plasmid p0157 DNA, complete sequence	2111	2111	100%	0.0	99%	
AF043470.1	Escherichia coli plasmid p0157 ecf4 gene, partial cds; and ecf3, ecf2, and ecf1 genes, complete cds	2102	2102	100%	0.0	99%	G
CP000035.1	Shigella dysenteriae Sd197 plasmid pSD1_197, complete sequence	138	138	24%	6e-29	71%	
CP001064.1	Escherichia coli 53638 plasmid p53638_226, complete sequence	132	132	24%	3e-27	71%	
CP001062.1	Shigella boydii CDC 3083-94 plasmid pBS512_211, complete sequence	132	132	24%	3e-27	71%	
AF386526.1	Shigella flexneri 2a str. 301 virulence plasmid pCP301, complete sequence	132	132	24%	3e-27	71%	
AY206446.1	Shigella flexneri plasmid pINV_F6_M1382 ORF186 (ORF186), VirK (virK), and MsbB2 (msbB2) genes, complete cds	132	132	24%	3e-27	71%	
AL391753.1	Shigella flexneri virulence plasmid pWR100: from 1 to 213494	132	132	24%	3e-27	71%	
AF348706.1	Shigella flexneri 5a plasmid virulence plasmid pWR501, complete sequence	132	132	24%	3e-27	71%	
AY879342.1	Shigella flexneri plasmid pSF5, complete sequence	132	132	24%	3e-27	71%	
CP000037.1	Shigella boydii Sb227 plasmid pSB4_227, complete sequence	132	132	24%	3e-27	71%	
CP000039.1	Shigella sonnei Ss046 plasmid pSS_046, complete sequence	132	132	24%	3e-27	71%	
D11025.1	Shigella flexneri plasmid pMYSH6000 virK gene for virulence protein, complete cds	132	132	24%	3e-27	71%	
CP000799.1	Escherichia coli E24377A plasmid pETEC_74, complete sequence	111	111	17%	9e-21	71%	
CP000795.1	Escherichia coli E24377A plasmid pETEC_80, complete sequence	111	111	17%	9e-21	71%	
AB255435.1	Escherichia coli plasmid p086A1 DNA, complete sequence	111	111	17%	9e-21	71%	
AF134403.1	Escherichia coli plasmid pAA2 Shf (shf), hexosyltransferase homolog (capU), and VirK (virK) genes, complete cds	111	111	17%	9e-21	71%	
CR942285.1	Escherichia coli plasmid pCoo	111	111	17%	9e-21	71%	
CP000800.1	Escherichia coli E24377A, complete genome	107	107	24%	1e-19	69%	
AC133908.7	Mus musculus chromosome 5, clone RP24-299L9, complete sequence	46.4	46.4	2%	0.30	93%	
AC127327.4	Mus musculus BAC clone RP23-254M18 from	46.4	46.4	2%	0.30	93%	

5, complete sequence

XU025714.1	<i>Salmo salar</i> retinoic acid receptor gamma a (Rarga), coiled-coil transcriptional coactivator a (Kiaa1536), homeobox protein HoxC13aa (HoxC13aa), homeobox protein HoxC12aa (HoxC12aa), homeobox protein HoxC11aa (HoxC11aa), homeobox protein HoxC10aa (HoxC10aa), homeobox protein HoxC9aa (HoxC9aa), homeobox protein HoxC8aa (HoxC8aa), and homeobox protein HoxC6aa (HoxC6aa) genes, complete cds	44.6	44.6	2%	1.1	93%	
BX571861.1	<i>Photorhabdus luminescens</i> subsp. laumondii TT01 complete genome; segment 3/17	44.6	44.6	2%	1.1	100%	
DQ192243.1	<i>Operophtera brumata</i> reovirus segment 9, complete sequence	42.8	42.8	2%	3.7	92%	G
AC145866.3	Pan troglodytes BAC clone RP43-21B7 from chromosome 7, complete sequence	42.8	42.8	2%	3.7	90%	
AE015928.1	<i>Bacteroides thetaiotaomicron</i> VPI-5482, complete genome	42.8	42.8	1%	3.7	100%	
AC004844.1	<i>Homo sapiens</i> PAC clone RP4-613I23 from 7p11-p13, complete sequence	42.8	42.8	2%	3.7	90%	E

Alignments

>gb|AF401292.1| **D** Escherichia coli O157:H- plasmid pSF0157, complete sequence
Length=121239

Score = 2111 bits (2340), Expect = 0.0
Identities = 1178/1182 (99%), Gaps = 1/1182 (0%)
Strand=Plus/Minus

Query	1	CTGCAGGAGA-TGG	TTGCCCATCCCAGCGCGCTCCAGCT	59
Sbjct	29247	CTGCAGGAGAGTGGAAAAAAGCCAAAATAAAAAATTGCCCATCCCAGCGCGCTCCAGCT		29
Query	60	GAAAGTAGGCCTGTTCTGTCCGGTATTTAAATGCATTGACCGTCCCGTATTTAAACAAT		11
Sbjct	29187	GAAAGTAGGCCTGTTCTGTCCGGTATTTAAATGCATTGACCGTCCCGTATTTAAACAAT		29
Query	120	GTGATAAATTACTCCGTTACCGGAAAACCGCTGAACAAAATTTCGGGCTGAAAAGAGGATC		17
Sbjct	29127	GTGATAAATTACTCCGTTACCGGAAAACCGCTGAACAAAATTTCGGGCTGAAAAGAGGATC		29
Query	180	CGCCGTTATCTGTTGCATTTCCCTTAGCCTGACTAGCCAGAGACACAATGATCTGTGCC		23
Sbjct	29067	CGCCGTTATCTGTTGCATTTCCCTTAGCCTGACTAGCCAGAGACACAATGATCTGTGCC		29
Query	240	GTTCTGTTAATATCAAACCGGTACTCAATATCTTCTCTGGCGCTGGCTGCCATCATCCGG		29
Sbjct	29007	GTTCTGTTAATATCAAACCGGTACTCAATATCTTCTCTGGCGCTGGCTGCCATCATCCGG		28
Query	300	AAGCGTTCCGGTCGGGATAAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACATCCCC		35
Sbjct	28947	AAGCGTTCCGGTCGGGATAAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACATCCCC		28
Query	360	ACGGGTAACAGCGTCCCTGTCACATTCTTCTGAATGACATCAGGGATCCCGCCCGTCTCA		41
Sbjct	28887	ACGGGTAACAGCGTCCCTGTCACATTCTTCTGAATGACATCAGGGATCCCGCCCGTCTCA		28
Query	420	CTGGCGATAACGGGCACGCCGAGACTGACGCTTCAGCCAGTACCATAACAAACGCTTCA		47
Sbjct	28827	CTGGCGATAACGGGCACGCCGAGACTGACGCTTCAGCCAGTACCATAACAAACGCTTCA		28
Query	480	TTTTCCGAAGGCATGACCACCACACTGGCAATCCGGTAGACCGGTAACGCTGGGAAAAGG		53
Sbjct	28767	TTTTCCGAAGGCATGACCACCACACTGGCAATCCGGTAGACCGGTAACGCTGGGAAAAGG		28
Query	540	GCACCTGCCATTAACACATCTCCGCTCATTCCCAGGTGTTCTGTCTGCTGACGCAGACGT		59
Sbjct	28707	GCACCTGCCATTAACACATCTCCGCTCATTCCCAGGTGTTCTGTCTGCTGACGCAGACGT		28
Query	600	GCTTCGTATTCTTCACGCCCGCGCCACCACGAGCCAGCGAAATGATTTCCCTTCCATC		65
Sbjct	28647	GCTTCGTATTCTTCACGCCCGCGCCACCACGAGCCAGCGAAATGATTTCCCTTCCATC		28
Query	660	TTCAGCTGATACAATACACGCAGCATAAATTCATGTCCTTTTTCGGGACGTAGCATCCCC		71
Sbjct	28587	TTCAGCTGATACAATACACGCAGCATAAATTCATGTCCTTTTTCGGGACGTAGCATCCCC		28
Query	720	ACCTGAACGATAAGCGGAACATTGTCTGCTGATGCAGCCCAGGCGTGGATATGCAGGGGT		77
Sbjct	28527	ACCTGAACGATAAGCGGAACATTGTCTGCTGATGCAGCCCAGGCGTGGATATGCAGGGGT		28
Query	780	AACGGTCGCATGGCTTCATTATGCAATGCGGGCCAGTCGAAACCCGGTGGAATAACCGTT		83
Sbjct	28467	AACGGTCGCATGGCTTCATTATGCAATGCGGGCCAGTCGAAACCCGGTGGAATAACCGTT		28
Query	840	ACCGGTGTCCTGACACCTTCCGCCATCAGATGCGCCATCATGGGTGAGATAGGCACAACA		89
Sbjct	28407	ACCGGTGTCCTGACACCTTCCGCCATCAGATGCGCCATCATGGGTGAGATAGGCACAACA		28
Query	900	ATGAAATCACACAGATAATTACGGGAAAACGTTCTGGTCTTACGGGTGATGTAGGTTTTT		95
Sbjct	28347	ATGAAATCACACAGATAATTACGGGAAAACGTTCTGGTCTTACGGGTGATGTAGGTTTTT		28
Query	960	TGTCTGACAATAGTGAAGCGGTGACAGCATATCAGACGGCTCAGTCCTGCTATATTACTG		10

Query	1	CTGCAGGAGA-TGGAGAGAGAGCTGAGAGAGAGTTGCCCATCCCAGCGCGCTCCAGCT	59
Sbjct	19435	CTGCAGGAGAGTGGAAAAAAGCCAAAATAAAAAATTGCCCATCCCAGCGCGCTCCAGCT	19
Query	60	GAAAGTAGGCCTGTTCTGTCCGGTATTTAAATGCATTGACCGTCCCCGTATTTAAACAAT	11
Sbjct	19375	GAAAGTAGGCCTGTTCTGTCCGGTATTTAAATGCATTGACCGTCCCCGTATTTAAACAAT	19
Query	120	GTGATAAATTACTCCGTTACCGGAAAACCGCTGAACAAAATTTCGGGCTGAAAAGAGGATC	17
Sbjct	19315	GTGATAAATTACTCCGTTACCGGAAAACCGCTGAACAAAATTTCGGGCTGAAAAGAGGATC	19
Query	180	CGCCGTTATCTGTTGCATTTCCCTTAGCCTGACTAGCCAGAGACACAATGATCTGTGCC	23
Sbjct	19255	CGCCGTTATCTGTTGCATTTCCCTTAGCCTGACTAGCCAGAGACACAATGATCTGTGCC	19
Query	240	GTTCTGTTAATATCAAACCGGTACTCAATATCTTCTCTGGCGCTGGCTGCCATCATCCGG	29
Sbjct	19195	GTTCTGTTAATATCAAACCGGTACTCAATATCTTCTCTGGCGCTGGCTGCCATCATCCGG	19
Query	300	AAGCGTTCGGGTCTGGGATAAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACATCCCC	35
Sbjct	19135	AAGCGTTCGGGTCTGGGATAAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACATCCCC	19
Query	360	ACGGGTAACAGCGTCCCTGTACATTCTTCTGAATGACATCAGGGATCCCGCCCGTCTCA	41
Sbjct	19075	ACGGGTAACAGCGTCCCTGTACATTCTTCTGAATGACATCAGGGATCCCGCCCGTCTCA	19
Query	420	CTGGCGATAACGGGCACGCCGAGACTGACGCTTCAGCCAGTACCATAACCAACGCTTCA	47
Sbjct	19015	CTGGCGATAACGGGCACGCCGAGACTGACGCTTCAGCCAGTACCATAACCAACGCTTCA	18
Query	480	TTTTCCGAAGGCATGACCACCACACTGGCAATCCGGTAGACCGGTAACGCTGGGAAAAGG	53
Sbjct	18955	TTTTCCGAAGGCATGACCACCACACTGGCAATCCGGTAGACCGGTAACGCTGGGAAAAGG	18
Query	540	GCACCTGCCATTAACACATCTCCGCTCATTTCCAGGTGTTCTGTCTGCTGACGCAGACGT	59
Sbjct	18895	GCACCTGCCATTAACACATCTCCGCTCATTTCCAGGTGTTCTGTCTGCTGACGCAGACGT	18
Query	600	GCTTCGTATTCTTTCACGCCCGGCGCCACCACGAGCCAGCGAAATGATTTCCCTTCCATC	65
Sbjct	18835	GCTTCGTATTCTTTCACGCCCGGCGCCACCACGAGCCAGCGAAATGATTTCCCTTCCATC	18
Query	660	TTCAGCTGATACAATACACGAGCATAAATTCATGTCCTTTTTTCGGGACGTAGCATCCCC	71
Sbjct	18775	TTCAGCTGATACAATACACGAGCATAAATTCATGTCCTTTTTTCGGGACGTAGCATCCCC	18
Query	720	ACCTGAACGATAAGCGGAACATTGTCTGCTGATGCAGCCCAGGCGTGGATATGCAGGGGT	77
Sbjct	18715	ACCTGAACGATAAGCGGAACATTGTCTGCTGATGCAGCCCAGGCGTGGATATGCAGGGGT	18
Query	780	AACGGTCGCATGGCTTCATTATGCAATGCGGGCCAGTCGAAACCCGGTGGAATAACCGTT	83
Sbjct	18655	AACGGTCGCATGGCTTCATTATGCAATGCGGGCCAGTCGAAACCCGGTGGAATAACCGTT	18
Query	840	ACCGGTGTCCTGACACCTTCCGCCATCAGATGCGCCATCATGGGTGAGATAGGCACAACA	89

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Query	1	CTGCAGGAGA-TGG	TTGCCCATCCCAGCGCGCTCCAGCT	59
Sbjct	88950	CTGCAGGAGAGTGAAAAAAGCCAAAATAAAAAATTGCCCATCCCAGCGCGCTCCAGCT		88
Query	60	GAAAGTAGGCCTGTTCTGTCCGGTATTTAAATGCATTGACCGTCCCCGTATTTAAACAAT		11
Sbjct	88890	GAAAGTAGGCCTGTTCTGTCCGGTATTTAAATGCATTGACCGTCCCCGTATTTAAACAAT		88
Query	120	GTGATAAATTACTCCGTTACCGGAAAACCGCTGAACAAAATTCCGGGCTGAAAAGAGGATC		17
Sbjct	88830	GTGATAAATTACTCCGTTACCGGAAAACCGCTGAACAAAATTCCGGGCTGAAAAGAGGATC		88
Query	180	CGCCGTTATCTGTTGCATTTCCCTTAGCCTGACTAGCCAGAGACACAATGATCTGTGCC		23
Sbjct	88770	CGCCGTTATCTGTTGCATTTCCCTTAGCCTGACTAGCCAGAGACACAATGATCTGTGCC		88
Query	240	GTTCTGTTAATATCAAACCGGTACTCAATATCTTCTCTGGCGCTGGCTGCCATCATCCGG		29
Sbjct	88710	GTTCTGTTAATATCAAACCGGTACTCAATATCTTCTCTGGCGCTGGCTGCCATCATCCGG		88
Query	300	AAGCGTTCGGGTCGGGATAAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACATCCCC		35
Sbjct	88650	AAGCGTTCGGGTCGGGATAAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACATCCCC		88
Query	360	ACGGGTAACAGCGTCCCTGTCACATTCTTCTGAATGACATCAGGGATCCCGCCCGTCTCA		41
Sbjct	88590	ACGGGTAACAGCGTCCCTGTCACATTCTTCTGAATGACATCAGGGATCCCGCCCGTCTCA		88
Query	420	CTGGCGATAACGGGCACGCCGAGACTGACGCTTCAGCCAGTACCATAACAAACGCTTCA		47
Sbjct	88530	CTGGCGATAACGGGCACGCCGAGACTGACGCTTCAGCCAGTACCATAACAAACGCTTCA		88
Query	480	TTTTCCGAAGGCATGACCACCACACTGGCAATCCGGTAGACCGGTAACGCTGGGAAAAGG		53
Sbjct	88470	TTTTCCGAAGGCATGACCACCACACTGGCAATCCGGTAGACCGGTAACGCTGGGAAAAGG		88
Query	540	GCACCTGCCATTAACACATCTCCGCTCATTCACAGGTGTTCTGTCTGCTGACGCAGACGT		59
Sbjct	88410	GCACCTGCCATTAACACATCTCCGCTCATTCACAGGTGTTCTGTCTGCTGACGCAGACGT		88

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Query 420 CTGGCGATAACGGGCACGCCGAGACTGACGCTTCAGCCAGTACCATAACCAAACGCTTCA 479
Sbjct 2824 CTGGCGATAACGGGCACGCCGAGACTGACGCTTCAGCCAGTACCATAACCAAACGCTTCA 288
Query 480 TTTTCCGAAGGCATGACCACCACACTGGCAATCCGGTAGACCGGTAACGCTGGGAAAAGG 539
Sbjct 2884 TTTTCCGAAGGCATGACCACCACACTGGCAATCCGGTAGACCGGTAACGCTGGGAAAAGG 294
Query 540 GCACCTGCCATTAACACATCTCCGCTCATTCCCAGGTGTTCTGTCTGCTGACGCAGACGT 599
Sbjct 2944 GCACCTGCCATTAACACATCTCCGCTCATTCCCAGGTGTTCTGTCTGCTGACGCAGACTT 300
Query 600 GCTTCGTATTCTTCACGCCCGGCGCCACCACGAGCCAGCGAAATGATTTCCCTTCCATC 659
Sbjct 3004 GCTTCGTATTCTTCACGCCCGGCGCCACCACGAGCCAGCGAAATGATTTCCCTTCCATC 306
Query 660 TTCAGCTGATACAATACACGCAGCATAAATTTCATGTCCTTTTTCGGGACGTAGCATCCCC 719
Sbjct 3064 TTCAGCTGATACAATACACGCAGCATAAATTTCATGTCCTTTTTCGGGACGTAGCATCCCC 312
Query 720 ACCTGAACGATAAGCGGAACATTGTCTGCTGATGCAGCCAGGCGTGGATATGCAGGGGT 779
Sbjct 3124 ACCTGAACGATAAGCGGAACATTGTCTGCTGATGCAGCCAGGCGTGGATATGCAGGGGT 318
Query 780 AACGGTCGCATGGCTTCATTATGCAATGCGGGCCAGTCGAAACCCGGTGGAAATACCGTT 839
Sbjct 3184 AACGGTCGCATGGCTTCATTATGCAATGCGGGCCAGTCGAAACCCGGTGGAAATACCGTT 324
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Sbjct 3244 ACCGGTGTCTCTGACACCTTCGCCCATCAGATGCGCCATCATGGGTGAGATAGGCACAACA 330
Query 900 ATGAAATCACACAGATAATTCAGGGAAAACGTTCTGGTCTTACGGGTGATGTAGGTTTTT 959
Sbjct 3304 ATGAAATCACACAGATAATTCAGGGAAAACGTTCTGGTCTTACGGGTGATGTAGGTTTTT 336
Query 960 TGTCTGACAATAGTGAAGCGGTGACAGCATATCAGACGGCTCAGTCCTGCTATATTACTG 101
Sbjct 3364 TGTCTGACAATACTGAAGCGGTGACAGCATATCAGACGGCTCAGTCCTGCTATATTACTG 342
Query 1020 TCATGGCCACTATGGCAGATGACCAGATCAGGTTTAAATTCCCCGATAATCCGTCGAAGT 107
Sbjct 3424 TCATGGCCACTATGGCAGATGACCAGATCAGGTTTAAATTCCCCGATAATCCGTCGAAGT 348
Query 1080 CTGAGGATGGAAGGAAGGTGAAGGCTGTTCTCTGAAAGGAATAAAAGTGACATCATGCCCT 113
Sbjct 3484 CTGAGGATGGAAGGAAGGTGAAGGCTGTTCTCTGAAAGGAATAAAAGTGACATCATGCCCT 354
Query 1140 CTTTTTCTGGCTTCCGGAGCAATTTTACTTTTTTCTCTGCAG 1181
Sbjct 3544 CTTTTTCTGGCTTCCGGAGCAATTTTACTTTTTTCTCTGCAG 3585

```

>gb|CP000035.1| **D** Shigella dysenteriae Sd197 plasmid pSD1_197, complete sequence
Length=182726

Score = 138 bits (152), Expect = 6e-29
Identities = 207/289 (71%), Gaps = 4/289 (1%)
Strand=Plus/Minus

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Query 237 GCCGTTCTGTAAATATCAAACCGGTACTCAATATCTTCTCTGGCGCTGGCT-GCCATCAT 29
Sbjct 87991 GCAGTTTTTATTAATATCAAACCGCTCTTCTATATCCTGTTTTGC-CTGGCGAGCCATCTG 87
Query 296 CCGGAAGCGTTCGG-TCGGGATAAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACAT 35
Sbjct 87932 ATAAAAACGTCCAGGGTCATTA-AAAAAATCATTACAGGGCGCACATCCATGCGTGCTTAT 87
Query 355 CCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTGAATGACATCAGGGATCCCGCCCG 41
Sbjct 87873 TACCTGCTGGTAACAATGTCCCGGTCTGGTTGTTCTGAATAACATCAGGGATTCACCAA 87
Query 415 TCTCACTGGCGATAACGGGCACGCCGAGACTGACGCTTCAGCCAGTACCATAACCAAACG 47
Sbjct 87813 TCTGACTGGCCAGTACAGGCACAGAAAATGCCGATGCTTCTGCCAGTACCATAACCAAACG 87
Query 475 CTTTATTTTCCGAAGGCATGACCACCACACTGGCAATCCGGTAGACCGG 523
Sbjct 87753 ATTCGTTTTCTGAAGGCAGAACACCAGACTGGCAACCCGATATACGGG 87705

```

>gb|CP001064.1| **D** Escherichia coli 53638 plasmid p53638_226, complete sequence
Length=225683

Features in this part of subject sequence:
UDP-sugar hydrolase

Score = 132 bits (146), Expect = 3e-27
Identities = 206/289 (71%), Gaps = 4/289 (1%)
Strand=Plus/Plus

```
Query 237      GCCGTTCTGTTAATATCAAACCGGTACTCAATATCTTCTCTGGCGCTGGCT-GCCATCAT 2
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 115503    GCAGTTTATTAATATCAAACCGCTCTTCTATATCCTGTTTGC-CTGGCGAGCCATCTG 1

Query 296      CCGGAAGCGTTCCGG-TCGGGATAAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACAT 3
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 115562    ATAAAAACGCCAGGGTCATTA-AAAAAATCATTCAGGGCGCACATCCATGCGTGCTTAT 1

Query 355      CCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTGAATGACATCAGGGATCCCGCCCG 4
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 115621    TACCTGCTGGTAACAATGTCCCGGTCTGGTTGTTCTGAATAACATCAGGGATTCCACCAA 1

Query 415      TCTCACTGGCGATAACGGGCACGCCGAGACTGACGCTTCAGCCAGTACCATAACAAACG 4
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 115681    TCTGACTGGCCAGTACAGGCACAGAAAATGCCGATGCTTCTGCCAGTACCATAACAAACG 1

Query 475      CTCATTTTCCGAAGGCATGACCACCACACTGGCAATCCGGTAGACCGG 523
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 115741    ATTCGTTTTCTGAAGGCAGAACCACCAGACTGGCAACCCGATATACGGG 115789
```

>gb|CP001062.1| **D** Shigella boydii CDC 3083-94 plasmid pBS512_211, complete sequence
Length=210919

Features in this part of subject sequence:
putative glycosyl transferase, group 1 family protein

Score = 132 bits (146), Expect = 3e-27
Identities = 206/289 (71%), Gaps = 4/289 (1%)
Strand=Plus/Minus

```
Query 237      GCCGTTCTGTTAATATCAAACCGGTACTCAATATCTTCTCTGGCGCTGGCT-GCCATCAT 2
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 176254    GCAGTTTATTAATATCAAACCGCTCTTCTATATCCTGTTTGC-CTGGCGAGCCATCTG 1

Query 296      CCGGAAGCGTTCCGG-TCGGGATAAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACAT 3
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 176195    ATAAAAACGCCAGGGTCATTA-AAAAAATCATTCAGGGCGCACATCCATGCGTGCTTAT 1

Query 355      CCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTGAATGACATCAGGGATCCCGCCCG 4
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 176136    TACCTGCTGGTAACAATGTCCCGGTCTGGTTGTTCTGAATAACATCAGGGATTCCACCAA 1

Query 415      TCTCACTGGCGATAACGGGCACGCCGAGACTGACGCTTCAGCCAGTACCATAACAAACG 4
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 176076    TCTGACTGGCCAGTACAGGCACAGAAAATGCCGATGCTTCTGCCAGTACCATAACAAACG 1

Query 475      CTCATTTTCCGAAGGCATGACCACCACACTGGCAATCCGGTAGACCGG 523
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 176016    ATTCGTTTTCTGAAGGCAGAACCACCAGACTGGCAACCCGATATACGGG 175968
```

>gb|AF386526.1| **D** Shigella flexneri 2a str. 301 virulence plasmid pCP301, complete sequence
Length=221618

Features in this part of subject sequence:
UDP-sugar hydrolase

Score = 132 bits (146), Expect = 3e-27
Identities = 206/289 (71%), Gaps = 4/289 (1%)
Strand=Plus/Minus

```
Query 237      GCCGTTCTGTTAATATCAAACCGGTACTCAATATCTTCTCTGGCGCTGGCT-GCCATCAT 2
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 193608    GCAGTTTATTAATATCAAACCGCTCTTCTATATCCTGTTTGC-CTGGCGAGCCATCTG 1

Query 296      CCGGAAGCGTTCCGG-TCGGGATAAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACAT 3
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21/07/2008

Features in this part of subject sequence:

UDP-sugar hydrolase

Score = 132 bits (146), Expect = 3e-27
 Identities = 206/289 (71%), Gaps = 4/289 (1%)
 Strand=Plus/Minus

```

Query  237      GCCGTTCTGTAAATATCAAACCGGTACTCAATATCTTCTCTGGCGCTGGCT-GCCATCAT  2
          || ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Sbjct  184956    GCAGTTTATTAAATATCAAACCGCTCTTCTATATCCTGTTTGC-CTGGCGAGCCATCTG  1

Query  296      CCGGAAGCGTTCCGG-TCGGGATAAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACAT  3
          || ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Sbjct  184897    ATAAAAACGCCCAGGGTCATTA-AAAAAATCATTAGGGGCGCACATCCATGCGTGCTTAT  1

Query  355      CCCCCACGGGTAACAGCGTCCCTGTACATTCTTCTGAATGACATCAGGGATCCCGCCCG  4
          || | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Sbjct  184838    TACCTGCTGGTAACAATGTCCCGGTCTGGTTATTCTGAATAACATCAGGGATTCCACCAA  1

Query  415      TCTCACTGGCGATAACGGGCACGCCGAGACTGACGCTTCAGCCAGTACCATAACCAAACG  4
          || | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Sbjct  184778    TCTGACTGGCCAGTACAGGCACAGAAAATGCCGATGCTTCTGCCAGTACCATAACCAAACG  1

Query  475      CTTCAATTTCCGAAGGCATGACCACCACACTGGCAATCCGGTAGACCGG  523
          || | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Sbjct  184718    ATTCGTTTTCTGAAGGCAGAACCACCAGACTGGCAACCCGATATACGGG  184670
  
```

>gb|AY879342.1| **D** Shigella flexneri plasmid pSF5, complete sequence
 Length=136694

Score = 132 bits (146), Expect = 3e-27
 Identities = 206/289 (71%), Gaps = 4/289 (1%)
 Strand=Plus/Plus

```

Query  237      GCCGTTCTGTAAATATCAAACCGGTACTCAATATCTTCTCTGGCGCTGGCT-GCCATCAT  29
          || ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Sbjct  62216    GCAGTTTATTAAATATCAAACCGCTCTTCTATATCCTGTGTTTGC-CTGGCGAGCCATCTG  62

Query  296      CCGGAAGCGTTCCGG-TCGGGATAAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACAT  35
          || ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Sbjct  62275    ATAAAAACGCCCAGGGTCATTA-AAAAAATCATTAGGGGCGCACATCCATGCGTGCTTAT  62

Query  355      CCCCCACGGGTAACAGCGTCCCTGTACATTCTTCTGAATGACATCAGGGATCCCGCCCG  41
          || | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Sbjct  62334    TACCTGCTGGTAACAATGTCCCGGTCTGGTTATTCTGAATAACATCAGGGATTCCACCAA  62

Query  415      TCTCACTGGCGATAACGGGCACGCCGAGACTGACGCTTCAGCCAGTACCATAACCAAACG  47
          || | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Sbjct  62394    TCTGACTGGCCAGTACAGGCACAGAAAATGCCGATGCTTCTGCCAGTACCATAACCAAACG  62

Query  475      CTTCAATTTCCGAAGGCATGACCACCACACTGGCAATCCGGTAGACCGG  523
          || | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Sbjct  62454    ATTCGTTTTCTGAAGGCAGAACCACCAGACTGGCAACCCGATATACGGG  62502
  
```

>gb|CP000037.1| **D** Shigella boydii Sb227 plasmid pSB4_227, complete sequence
 Length=126697

Score = 132 bits (146), Expect = 3e-27
 Identities = 206/289 (71%), Gaps = 4/289 (1%)
 Strand=Plus/Minus

```

Query  237      GCCGTTCTGTAAATATCAAACCGGTACTCAATATCTTCTCTGGCGCTGGCT-GCCATCAT  29
          || ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Sbjct  98146    GCAGTTTATTAAATATCAAACCGCTCTTCTATATCCTGTTTGC-CTGGCGAGCCATCTG  98

Query  296      CCGGAAGCGTTCCGG-TCGGGATAAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACAT  35
          || ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Sbjct  98087    ATAAAAACGCCCAGGGTCATTA-AAAAAATCATTAGGGGCGCACATCCATGCGTGCTTAT  98

Query  355      CCCCCACGGGTAACAGCGTCCCTGTACATTCTTCTGAATGACATCAGGGATCCCGCCCG  41
          || | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Sbjct  98028    TACCTGCTGGTAACAATGTCCCGGTCTGGTTGTTCTGAATAACATCAGGGATTCCACCAA  97

Query  415      TCTCACTGGCGATAACGGGCACGCCGAGACTGACGCTTCAGCCAGTACCATAACCAAACG  47
          || | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Sbjct  97968    TCTGACTGGCCAGTACAGGCACAGAAAATGCCGATGCTTCTGCCAGTACCATAACCAAACG  97

Query  475      CTTCAATTTCCGAAGGCATGACCACCACACTGGCAATCCGGTAGACCGG  523
  
```

Sbjct 97908 ATTCGTTTTCTGAAGGCAGAACACCAGACTGGCAACCCGATATACGGG 97860

>gb|CP000039.1| **D** Shigella sonnei Ss046 plasmid pSS_046, complete sequence
Length=214396

Features in this part of subject sequence:
conserved hypothetical protein

Score = 132 bits (146), Expect = 3e-27
Identities = 206/289 (71%), Gaps = 4/289 (1%)
Strand=Plus/Minus

```

Query 237   GCCGTTCTGTAAATATCAAACCGGTACTCAATATCTTCTCTGGCGCTGGCT-GCCATCAT 2
           ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 158570 GCAGTTTTATTAATATCAAACCGCTCTTCTATATCCTGTTTGC-CTGGCGAGCCATCTG 1

Query 296   CCGGAAGCGTTCCGG-TCGGGATAAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACAT 3
           ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 158511 ATAAAAACGCCAGGGTCATTA-AAAAAATCATTTCAGGGCGCACATCCATGCGTGCTTAT 1

Query 355   CCCCCACGGGTAACAGCGTCCCTGTACATTCTTCTGAATGACATCAGGGATCCCGCCCG 4
           ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 158452 TACCTGCTGGTAACAATGTCCCGGTCTGGTTGTTCTGAATAACATCAGGGATTCCACCAA 1

Query 415   TCTCACTGGCGATAACGGGCACGCCGAGACTGACGCTTCAGCCAGTACCATAACCAAACG 4
           ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 158392 TCTGACTGGCCAGTACAGGCACAGAAAATGCCGATGCTTCTGCCAGTACCATAACCAAACG 1

Query 475   CTTCATTTTCCGAAGGCATGACCACCACACTGGCAATCCGGTAGACCGG 523
           ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 158332 ATTCGTTTTCTGAAGGCAGAACACCAGACTGGCAACCCGATATACGGG 158284

```

>dbj|D11025.1| **SHEFVIRK** Shigella flexneri plasmid pMYSH6000 virK gene for virul.
complete cds
Length=1642

Score = 132 bits (146), Expect = 3e-27
Identities = 206/289 (71%), Gaps = 4/289 (1%)
Strand=Plus/Minus

```

Query 237   GCCGTTCTGTAAATATCAAACCGGTACTCAATATCTTCTCTGGCGCTGGCT-GCCATCAT 295
           ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 334   GCAGTTTTATTAATATCAAACCGCTCTTCTATATCCTGTTTGC-CTGGCGAGCCATCTG 276

Query 296   CCGGAAGCGTTCCGG-TCGGGATAAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACAT 354
           ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 275   ATAAAAACGCCAGGGTCATTA-AAAAAATCATTTCAGGGCGCACATCCATGCGTGCTTAT 217

Query 355   CCCCCACGGGTAACAGCGTCCCTGTACATTCTTCTGAATGACATCAGGGATCCCGCCCG 414
           ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 216   TACCTGCTGGTAACAATGTCCCGGTCTGGTTATTCTGAATAACATCAGGGATTCCACCAA 157

Query 415   TCTCACTGGCGATAACGGGCACGCCGAGACTGACGCTTCAGCCAGTACCATAACCAAACG 474
           ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 156   TCTGACTGGCCAGTACAGGCACAGAAAATGCCGATGCTTCTGCCAGTACCATAACCAAACG 97

Query 475   CTTCATTTTCCGAAGGCATGACCACCACACTGGCAATCCGGTAGACCGG 523
           ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 96    ATTCGTTTTCTGAAGGCAGAACACCAGACTGGCAACCCGATATACGGG 48

```

>gb|CP000799.1| **D** Escherichia coli E24377A plasmid pETEC_74, complete sequence
Length=74224

Score = 111 bits (122), Expect = 9e-21
Identities = 148/206 (71%), Gaps = 0/206 (0%)
Strand=Plus/Minus

```

Query 318   AAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACATCCCCACGGGTAACAGCGTCCCT 37
           ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 61325   AAAAAATCATTTCAGGGCGCACATCCATGCGTGCTTATTACCTGCTGGTAACAATGTCCCG 61

Query 378   GTCACATTCTTCTGAATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACG 43
           ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 61265   GTCTGGTTGTTCTGAATAACCTCAGGGATTCCACCAATCTGAGTGGCCACTACAGGCACA 61

Query 438   CCGGAGACTGACGCTTCAGCCAGTACCATAACCAAACGCTTCATTTTCCGAAGGCATGACC 49


```

Sbjct	61205	GAA	AAT	TG	CC	GAT	GCT	TCT	TG	CC	AG	CAC	CA	TAC	CA	AA	A	G	AT	T	C	G	T	T	T	T	C	T	G	A	A	G	G	C	A	A	C	61
Query	498	ACC	CA	CT	TG	GC	AA	TC	CG	TA	GA	CC	GG	523																								
Sbjct	61145	ACC	CA	CT	TG	GC	AA	CC	GA	TAT	AC	GG	61120																									

```
>gb|CP000795.1|  Escherichia coli E24377A plasmid pETEC_80, complete sequence  
Length=79237
```

Score = 111 bits (122), Expect = 9e-21
Identities = 148/206 (71%), Gaps = 0/206 (0%)
Strand=Plus/Plus

Query	318	AAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACATCCCCACGGGTAACAGCGTCCCT	37
Sbjct	37177	AAAAAATCATTTCAGGGCGCACATCCATGCGTGCTTATTACCTGCTGGTAACAATGTCCCG	37
Query	378	GTCACATTCTTCTGAATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACG	43
Sbjct	37237	GTCTGGTTGTTCTGAATAACCTCAGGGATTCCACCAATCTGAGTGGCCACTACAGGCACA	37
Query	438	CCGGAGACTGACGCTTCAGCCAGTACCATAACCAAACGCTTCATTTTCCGAAGGCATGACC	49
Sbjct	37297	GAAATGCCGATGCTTCTGCCAGCACCATAACCAAAAGATTTCGTTTTCTGAAGGCAGAACC	37
Query	498	ACCACACTGGCAATCCGGTAGACCGG	523
Sbjct	37357	ACCAGACTGGCAACCCGATATACGGG	37382

```
>dbj|AB255435.1|  Escherichia coli plasmid pO86A1 DNA, complete sequence
Length=120730
```

Score = 111 bits (122), Expect = 9e-21
Identities = 148/206 (71%), Gaps = 0/206 (0%)
Strand=Plus/Plus

Query	318	AAAAAATCGCGCAGTGC	CGCCGGTCCATGCAGACACATCCCCACGGGTAA	CAGCGTCCCT	377
Sbjct	2154	AAAAAATCATT	CAGGGCGCACATCCATGCGTGCTTATTACCTGCTGGTAACAATGTCCCG		221
Query	378	GTCACATTCTTCTGAATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACG		437	
Sbjct	2214	GTCTGGTTGTTCTGAATAACCTCAGGGATTCCACCAATCTGAGTGGCCACTACAGGCACA		227	
Query	438	CCGGAGACTGACGCTTCAGCCAGTACCATAACAAACGCTTCATTTTCCGAAGGCATGACC		497	
Sbjct	2274	GAAAATGCCGATGCTTCTGCCAGCACCATACCAAAAGATTCTGTTTTCTGAAGGCAGAACC		233	
Query	498	ACCACACTGGCAATCCGGTAGACCGG	523		
Sbjct	2334	ACCAGACTGGCAACCCGATATACGGG	2359		

>**gb|AF134403.1|AF134403** Escherichia coli plasmid pAA2 Shf (shf), hexosyltrans (capU), and VirK (virK) genes, complete cds
Length=3500

Score = 111 bits (122), Expect = 9e-21
Identities = 148/206 (71%), Gaps = 0/206 (0%)
Strand=Plus/Minus

Query	318	AAAAAATCGCGCAGTGC	CGCCGGTCCATGCAGACACATCCCCACGGGTAACAGCGTCCCT	377
Sbjct	2333	AAAAAATCATTCA	GGGCGCACATCCATGCGTGCTTATTACCTGCTGGTAACAATGTCCCG	227
Query	378	GTCACATTCTTCTGAATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACG	437	
Sbjct	2273	GTCTGGTTGTTCTGAATAACCTCAGGGATTCCACCAATCTGAGTGGCCACTACAGGCACA	221	
Query	438	CCGGAGACTGACGCTTCAGCCAGTACCATAACCAAACGCTTCATTTTCCGAAGGCATGACC	497	
Sbjct	2213	GAAAATGCCGATGCTTCTGCCAGCACCATACCAAAAGATTTCGTTTTCTGAAGGCAGAACC	215	
Query	498	ACCACACTGGCAATCCGGTAGACCGG	523	
Sbjct	2153	ACCAGACTGGCAACCCGATATACGGG	2128	

>emb|CR942285.1| **D** Escherichia coli plasmid pCoo
Length=98396

Score = 111 bits (122), Expect = 9e-21
Identities = 148/206 (71%), Gaps = 0/206 (0%)
Strand=Plus/Plus

```
Query 318      AAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACATCCCCACGGGTAACAGCGTCCCT 37
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 34153     AAAAAATCATTTCAGGGCGCACATCCATGCGTGCTTATTACCTGCTGGTAACAATGTCCCG 34

Query 378      GTCACATTCTTCTGAATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACG 43
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 34213     GTCTGGTTGTTCTGAATAACCTCAGGGATTCCACCAATCTGAGTGGCCACTACAGGCACA 34

Query 438      CCGGAGACTGACGCTTCAGCCAGTACCATAACAAACGCTTCATTTTCCGAAGGCATGACC 49
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 34273     GAAAATGCCGATGCTTCTGCCAGCACCATAACAAAAGATTGCTTTTCTGAAGGCAGAACC 34

Query 498      ACCACACTGGCAATCCGGTAGACCGG 523
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 34333     ACCAGACTGGCAACCCGATATACGGG 34358
```

>gb|CP000800.1| **D** Escherichia coli E24377A, complete genome
Length=4979619

Features in this part of subject sequence:
putative glycosyl transferase, group 1 family protein

Score = 107 bits (118), Expect = 1e-19
Identities = 201/290 (69%), Gaps = 4/290 (1%)
Strand=Plus/Plus

```
Query 236      TGCCGTTCTGT'TAATATCAAACCGGTACTCAATATCTTCTCTGGCGCTGGCT-GCCATCA
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 4845818   TGCAGTTTAT'TAATATCAAACCGCTCTTCTATATCCTGTTTTC-CAGGCGAGCCATCT

Query 295      TCCGGAAGCGTTCCGG-TCCGGATAAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACA
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 4845877   GATAAAAACGCCAGGGTCATTA-AAAAAATCATTAGGGCGCACATCCATGCGTGCTTA

Query 354      TCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTGAATGACATCAGGGATCCCGCCC
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 4845936   TTACTTGCTGGTAACAATGTCCCGGTCTGGT'TG'TTCTGAATAACCTCAGGGATTCCACCA

Query 414      GTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATAACAAAC
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 4845996   ATCTGAGTGGCCACTACAGGCACAGAAAATGCCGATGCTTCTGCCAGCACCATACCAAAA

Query 474      GCTTCATTTTCCGAAGGCATGACCACCACACTGGCAATCCGGTAGACCGG 523
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 4846056   GATTGTTTTTCTGAAGGCAGAACACCAGACTGGCAACCCGATATACGGG 4846105
```

>gb|AC133908.7| **D** Mus musculus chromosome 5, clone RP24-299L9, complete sequence
Length=214270

Score = 46.4 bits (50), Expect = 0.30
Identities = 28/30 (93%), Gaps = 0/30 (0%)
Strand=Plus/Minus

```
Query 4      CAGGAGATGGAAAAAAGCCAAAATAAAAA 33
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 185462   CAGGAGATGGAAAAAAGCTGAAATAAAAA 185433
```

>gb|AC127327.4| **D** Mus musculus BAC clone RP23-254M18 from 5, complete sequence
Length=198433

Score = 46.4 bits (50), Expect = 0.30
Identities = 28/30 (93%), Gaps = 0/30 (0%)
Strand=Plus/Minus

```
Query 4      CAGGAGATGGAAAAAAGCCAAAATAAAAA 33
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 92692   CAGGAGATGGAAAAAAGCTGAAATAAAAA 92663
```

>gb|EU025714.1| **D** Salmo salar retinoic acid receptor gamma a (Rarga), coiled-transcriptional coactivator a (Kiaal536), homeobox protein HoxC13aa (HoxC13aa), homeobox protein HoxC12aa (HoxC12aa), homeobox protein HoxC11aa (HoxC11aa), homeobox protein HoxC10aa (HoxC10aa), homeobox protein HoxC9aa (HoxC9aa), homeobox protein HoxC8aa (HoxC8aa), and homeobox protein HoxC6aa (HoxC6aa) genes, complete cds
Length=212839

Features in this part of subject sequence:
retinoic acid receptor gamma a

Score = 44.6 bits (48), Expect = 1.1
Identities = 27/29 (93%), Gaps = 0/29 (0%)
Strand=Plus/Plus

Query	1077	AGTCTGAGGATGGAAGGAAGGTGAAGGCT	1105
Sbjct	31660	AGTATGAGGATGGAAGGAAGGTGAGGGCT	31688

```
>emb|BX571861.1| D Photorhabdus luminescens subsp. laumondii TT01 complete ge:
segment 3/17
Length=342905
```


Features in this part of subject sequence:
unnamed protein product

Score = 44.6 bits (48), Expect = 1.1
Identities = 24/24 (100%), Gaps = 0/24 (0%)
Strand=Plus/Minus

```

Query    20      agpctgacacTTGCCCATC 43
          |||||
Sbjct   27988 AGCCAAAATAAAAAATTGCCCATC 27965

```

>gb|DQ192243.1|  Operophtera brumata reovirus segment 9, complete sequence
Length=1547


GENE ID: 5076725 OBRV_s9gp1 | hypothetical protein
[Operophtera brumata reovirus]

Score = 42.8 bits (46), Expect = 3.7
Identities = 26/28 (92%), Gaps = 0/28 (0%)
Strand=Plus/Minus

```

Query 247 TAATATCAAACCGGTACTCAATATCTTC 274
      |||||
Sbjct 260 TAATATCAAACCGGTATTCAATACCTTC 233

```


```
>gb|AC145866.3|  Pan troglodytes BAC clone RP43-21B7 from chromosome 7, comp
sequence
Length=189814
```

Score = 42.8 bits (46), Expect = 3.7
Identities = 28/31 (90%), Gaps = 0/31 (0%)
Strand=Plus/Plus

```

Query  366      AACAGCGTCCCTGTCACATTCTTCTGAATGA      396
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct  137128    AACAGAGTCCCTTTCACATCCTTCTGAATGA      137158

```

>gb|AE015928.1|  Bacteroides thetaiotaomicron VPI-5482, complete genome
Length=6260361

Features in this part of subject sequence:
Histone-like bacterial DNA-binding protein

Score = 42.8 bits (46), Expect = 3.7
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

Query 855 CCTTCCGCCATCAGATGCGCCAT 877


```
|||||
Sbjct  6023752 CCTTCGCCATCAGATGCGCCAT 6023774
```

>gb|AC004844.1| **ED** Homo sapiens PAC clone RP4-613I23 from 7p11-p13, complete
Length=141895

Score = 42.8 bits (46), Expect = 3.7
Identities = 28/31 (90%), Gaps = 0/31 (0%)
Strand=Plus/Plus

```
Query   366      AACAGCGTCCCTGTACAA'TTCTTCTGAATGA   396
          ||||| ||||| ||||| ||||| |||||
Sbjct  110633 AACAGAGTCCCTTTTACATCCTTCTGAATGA 110663
```

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS,
GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)

Posted date: Jul 20, 2008 5:48 PM

Number of letters in database: -1,464,584,741

Number of sequences in database: 7,064,549

Lambda	K	H
0.634	0.408	0.912

Gapped

Lambda	K	H
0.634	0.408	0.912

Matrix: blastn matrix:2 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 7064549

Number of Hits to DB: 12224137

Number of extensions: 604140

Number of successful extensions: 8350

Number of sequences better than 10: 0

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 8350

Number of HSP's successfully gapped: 0

Length of query: 1181

Length of database: 24305219031

Length adjustment: 36

Effective length of query: 1145

Effective length of database: 24050895267

Effective search space: 27538275080715

Effective search space used: 27538275080715

A: 0

X1: 22 (20.1 bits)

X2: 33 (29.8 bits)

X3: 110 (99.2 bits)

S1: 29 (27.4 bits)

S2: 45 (41.9 bits)